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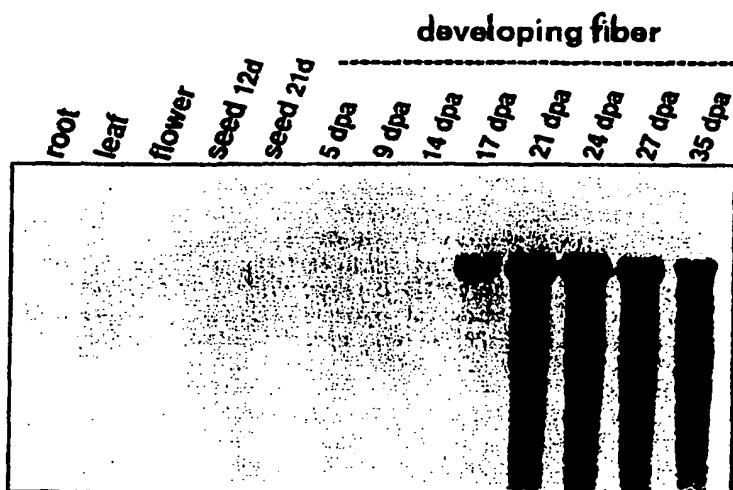
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(71) Applicant (for all designated States except US): CALGENE, INC. [US/US]; 1920 Fifth Street, Davis, CA 95616 (US).			
(72) Inventors; and			
(75) Inventors/Applicants (for US only): STALKER, David, M. [US/US]; 870 W. Southwood, Woodland, CA 95695 (US). PEAR, Julie, R. [US/US]; 818 Douglass Avenue, Davis, CA 95616 (US). DELMER, Deborah, P. [US/US]; 29 West Mill Street, New Palestine, IN 46163 (US).			
(74) Agents: SCHWEDLER, Carl, J. et al.; Calgene, Inc., 1920 Fifth Street, Davis, CA 95616 (US).			

(54) Title: PLANT CELLULOSE SYNTHASE AND PROMOTER SEQUENCES

(57) Abstract

Provided are two plant cDNA clones that are homologs of the bacterial CelA genes that encode the catalytic subunit of cellulose synthase, derived from cotton (*Gossypium hirsutum*). Also provided are genomic promoter regions to these encoding regions to cellulose synthase. Methods for using cellulose synthase in cotton fiber and wood quality modification are also provided.



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PLANT CELLULOSE SYNTHASE AND PROMOTER SEQUENCES

5

INTRODUCTIONTechnical Field

This invention relates to plant cellulose synthase cDNA encoding sequences, and their use in modifying plant phenotypes. Methods are provided whereby the sequences can be 10 used to control or limit the expression of endogenous cellulose synthase.

This invention also relates to methods of using *in vitro* constructed DNA transcription or expression cassettes capable of directing fiber-tissue transcription of a DNA sequence of 15 interest in plants to produce fiber cells having an altered phenotype, and to methods of providing for or modifying various characteristics of cotton fiber. The invention is exemplified by methods of using cotton fiber promoters for altering the phenotype of cotton fiber, and cotton fibers 20 produced by the method.

Background

In spite of much effort, no one has succeeded in isolating and characterizing the enzyme(s) responsible for 25 synthesis of the major cell wall polymer of plants, cellulose.

Numerous efforts have been directed toward the study of synthesis of cellulose (1,4- β -D-glucan) in higher plants. However, hampered by low rates of activity *in vitro*, the cellulose synthase of plants has resisted purification and 30 detailed characterization (for reviews, see 1,2). Aided by the discovery of cyclic-di-GMP as a specific activator, the cellulose synthase of the bacterium *Acetobacter xylinum* can be easily assayed *in vitro*, has been purified to homogeneity, and a catalytic subunit identified (for reviews, see 2,3). Furthermore, an operon of four genes involved in cellulose 35 synthesis in *A. xylinum* has been cloned (4-7).

Characterization of these genes indicates that the first gene, termed either *BcsA* (7) or *AcsAB* (6) codes for the 83 kD

subunit of the cellulose synthase that binds the substrate UDP-glc and presumably catalyzes the polymerization of glucose residues to 1,4- β -D-glucan (8). The second gene (B) of the operon is believed to function as a regulatory subunit binding cyclic-di-GMP (9) while recent evidence suggests that the C and D genes may code for proteins that form a pore allowing secretion of the polymer and control the pattern of crystallization of the resulting microfibrils (6).

Agrobacterium tumefaciens, have also led to cloning of genes involved in cellulose synthesis (10,11), although the proposed pathway of synthesis differs in some respects from that of *A. xylinum*. In *A. tumefaciens*, a CelA gene showing significant homology to the BcsA/AcsAB gene of *A. xylinum*, is proposed to transfer glc from UDP-glc to a lipid acceptor; other gene products may then build up a lipid oligosaccharide that is finally polymerized to cellulose by the action of an endo-glucanase functioning in a synthetic mode. In addition, homologs of the CelA, B, and C genes have been identified in *E. coli*, but, as this organism is not known to synthesize cellulose *in vivo*, the function of these genes is not clear (2).

These successes in bacterial systems opened the possibility that homologs of the bacterial genes might be identified in higher plants. However, experiments in a number of laboratories utilizing the *A. xylinum* genes as probes for screening plant cDNA libraries have failed to identify similar plant genes. Such lack of success suggests that, if plants do contain homologs of the bacterial genes, their overall sequence homology is not very high. Recent studies analyzing the conserved motifs common to glycosyltransferases using either UDP-glc or UDP-GlcNAc as substrate suggest that there are specific conserved regions that might be expected to be found in any plant homolog of the catalytic subunit (referred to hereafter as CelA). In one of these studies, Delmer and Amor (2) identified a motif common to many such glycosyltransferases including the bacterial CelA proteins.

An independent analysis (6) also concluded that this motif was highly conserved in a group of similar glycosyltransferases.

Extending these studies further, Saxena et al. (12) presented an elegant model for the mechanism of catalysis for enzymes such as cellulose synthase that have the unique problem of synthesizing consecutive residues that are rotated approximately rotated 180° with respect to each other. The model invokes independent UDP-glc binding sites and, based upon hydrophobic cluster analysis of these enzymes, the authors concluded that 3 critical regions in all such processive glycosyltransferases each contain a conserved aspartate (D) residue, while a fourth region contained a conserved QXXRW motif. The first D residue resides in the motif as previously analyzed (2,6).

In general, genetic engineering techniques have been directed to modifying the phenotype of individual prokaryotic and eukaryotic cells, especially in culture. Plant cells have proven more intransigent than other eukaryotic cells, due not only to a lack of suitable vector systems but also as a result of the different goals involved. For many applications, it is desirable to be able to control gene expression at a particular stage in the growth of a plant or in a particular plant part. For this purpose, regulatory sequences are required which afford the desired initiation of transcription in the appropriate cell types and/or at the appropriate time in the plant's development without having serious detrimental effects on plant development and productivity. It is therefore of interest to be able to isolate sequences which can be used to provide the desired regulation of transcription in a plant cell during the growing cycle of the host plant.

One aspect of this interest is the ability to change the phenotype of particular cell types, such as differentiated epidermal cells that originate in fiber tissue, i.e. cotton fiber cells, so as to provide for altered or improved aspects of the mature cell type. Cotton is a plant of great commercial significance. In addition to the use of cotton fiber in the production of textiles, other uses of cotton

include food preparation with cotton seed oil and animal feed derived from cotton seed husks.

A related goal involving the control of cell wall and characteristics would be to affect valuable secondary tree characteristics of wood for paper forestry products. For instance, by altering the balance of cellulose and lignin, the quality of wood for paper production may be improved.

Finally, despite the importance of cotton as a crop, the

10 has taken place at a relatively slow rate because of the absence of reliable promoters for use in selectively effecting changes in the phenotype of the fiber. In order to effect the desired phenotypic changes, transcription initiation regions capable of initiating transcription in fiber cells during
15 development are desired. Thus, an important goal of cotton bioengineering research is the acquisition of a reliable promoter which would permit expression of a protein selectively in cotton fiber to affect such qualities as fiber strength, length, color and dyability.

Relevant Literature

Cotton fiber-specific promoters are discussed in PCT publications WO 94/12014 and WO 95/08914, and John and Crow, Proc. Natl. Acad. Sci. USA, 89:5769-5773, 1992. cDNA clones that are preferentially expressed in cotton fiber have been isolated. One of the clones isolated corresponds to mRNA and protein that are highest during the late primary cell wall and early secondary cell wall synthesis stages. John and Crow, *supra*.

In plants, control of cytoskeletal organization is poorly understood in spite of its importance for the regulation of patterns of cell division, expansion, and subsequent deposition of secondary cell wall polymers. The cotton fiber represents an excellent system for studying cytoskeletal organization. Cotton fibers are single cells in which cell elongation and secondary wall deposition can be studied as distinct events. These fibers develop synchronously within the boll following anthesis, and each fiber cell elongates for

about 3 weeks, depositing a thin primary wall (Meinert and Delmer, (1984) *Plant Physiol.* 59: 1088-1097; Basra and Malik, (1984) *Int Rev of Cytol* 89: 65-113). At the time of transition to secondary wall cellulose synthesis, the fiber 5 cells undergo a synchronous shift in the pattern of cortical microtubule and cell wall microfibril alignments, events which may be regulated upstream by the organization of actin (Seagull, (1990) *Protoplasma* 159: 44-59; and (1992) In: *Proceedings of the Cotton Fiber Cellulose Conference*, National 10 Cotton Council of America, Memphis TN, pp 171-192.

Agrobacterium-mediated cotton transformation is described in Umbeck, United States Patents Nos. 5,004,863 and 5,159,135 and cotton transformation by particle bombardment is reported in WO 92/15675, published September 17, 1992. Transformation 15 of *Brassica* has been described by Radke et al. (*Theor. Appl. Genet.* (1988) 75:685-694; *Plant Cell Reports* (1992) 11:499-505.

Genes involved in lignin biosynthesis are described by Dwivedi, U.N., Campbell, W.H., Yu, J., Datla, R.S.S., Chiang, 20 V.L., and Podila, G.K. (1994) "Modification of lignin biosynthesis in transgenic Nicotiana through expression of an antisense O-methyltransferase gene from *Populus*" *Pl. Mol. Biol.* 26: 61-71; and Tsai, C.J., Podila, G.K. and Chaing, V.L. (1995) "Nucleotide sequence of *Populus tremuloides* gene for 25 caffeic acid/5 hydroxyferulic acid O-methyltransferase" *Pl. Physiol.* 107: 1459; and also U.S. Patent No. 5,451,514 (claiming the use of cinnamyl alcohol dehydrogenase gene in an antisense orientation such that the endogenous plant cinnamyl alcohol dehydrogenase gene is inhibited).

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SUMMARY OF THE INVENTION

Two cotton genes, CelA1 and CelA2, have been shown to be highly expressed in developing fibers at the onset of secondary wall cellulose synthesis. Comparisons indicate that these genes and the rice CelA gene encode polypeptides that have three regions of reasonably high homology, both in terms of primary amino acid sequence and hydropathy, with bacterial CelA proteins. The fact that these homologous stretches are in the same sequential order as in the bacterial CelA proteins and also contain four sub-regions previously predicted to be critical for substrate binding and catalysis (12) argues that the plant genes encode true homologs of bacterial CelA proteins. Furthermore, the pattern of expression in fiber as well as our demonstration that at least one of these highly-conserved regions is critical for UDP-glc binding also supports this conclusion.

30 Novel DNA promoter sequences are also supplied, and methods for their use are described for directing transcription of a gene of interest in cotton fiber.

The developing cotton fiber is an excellent system for studies on cellulose synthesis as these single cells develop synchronously in the boll and, at the end of elongation, 35 initiate the synthesis of a nearly pure cellulosic cell wall. During this transition period, synthesis of other cell wall polymers ceases and the rate of cellulose synthesis is estimated to rise nearly 100-fold *in vivo* (13). In our

continuing efforts to identify genes critical to this phase of fiber development, we have initiated a program sequencing randomly selected cDNA clones derived from a library prepared from mRNA harvested from fibers at the stage in which 5 secondary wall synthesis approaches its maximum rate (approximately 21 dpa).

We have characterized two cotton (*Gossypium hirsutum*)

are homologs of the bacterial CelA genes that encode the 10 catalytic subunit of cellulose synthase. Three regions in the deduced amino acid sequences of the plant CelA gene products are conserved with respect to the proteins encoded by bacterial CelA genes. Within these conserved regions are four highly conserved subdomains previously suggested to be 15 critical for catalysis and/or binding of the substrate UDP-glc. An overexpressed DNA segment of the cotton CelA1 gene encodes a polypeptide fragment that spans these domains and effectively binds UDP-glc, while a similar fragment having one of these domains deleted does not. The plant CelA genes 20 show little homology at the amino and carboxy terminal regions and also contain two internal insertions of sequence, one conserved and one hypervariable, that are not found in the bacterial gene sequences. Cotton CelA1 and CelA2 genes are expressed at high levels during active secondary wall 25 cellulose synthesis in the developing fiber. Genomic Southern analyses in cotton demonstrate that CelA comprises a family of approximately four distinct genes.

We report here the discovery of two cotton genes that show highly-enhanced expression at the time of onset of 30 secondary wall synthesis in the fiber. The sequences of these two cDNA clones, termed CelA1 and CelA2, while not identical, are highly homologous to each other and to a sequenced rice EST clone discovered in the dBEST databank. The deduced 35 proteins also share significant regions of homology with the bacterial CelA proteins. Coupled with their high level and specificity of expression in fiber at the time of active cellulose synthesis, as well as the ability of an *E. coli* expressed fragment of the CelA1 gene product to bind UDP-glc,

these findings support the conclusion that these plant genes are true homologs of the bacterial CelA genes.

The methods of the present invention include transfecting a host plant cell of interest with a transcription or expression cassette comprising a cotton fiber promoter and generating a plant which is grown to produce fiber having the desired phenotype. Constructs and methods of the subject invention thus find use in modulation of endogenous fiber products, as well as production of exogenous products and in modifying the phenotype of fiber and fiber products. The constructs also find use as molecular probes. In particular, constructs and methods for use in gene expression in cotton embryo tissues are considered herein. By these methods, novel cotton plants and cotton plant parts, such as modified cotton fibers, may be obtained.

The sequences and constructs of this invention may also be used to isolate related cellulose synthase genes from forest tree species, for use in transforming and modifying wood quality. As an example, lignin, an undesirable by-product of the pulping process, may be reduced by over-expressing the cellulose synthase product and diverting production into cellulose.

Thus, the application provides constructs and methods of use relating to modification of cell and cell wall phenotype in cotton fiber and wood products.

DESCRIPTION OF THE DRAWINGS

Figure 1. Northern analysis of CelA1 gene in cotton tissues and developing fiber. Approximately 10 μ g total RNA from each tissue was loaded per lane. Blots were prepared and probe preparation and hybridization conditions were performed as described previously (14). The entire CelA1 cDNA insert was used as a probe in this experiment. Exposure time for the autoradiogram was seven hours at -70°.

Figure 2. Cotton genomic DNA analysis for both the CelA1 and CelA2 cDNAs. Approximately 10-12 μ g of DNA was digested with the designated restriction enzymes and electrophoresed 0.9% agarose gels. Probe preparation and hybridization conditions were as described previously (14).

The entire CelA1 and CelA2 cDNAs were utilized as probes.

Exposure time for the autoradiograms was three days at -70°.

Figure 3. Multiple alignment of deduced amino acid sequences of plant and bacterial CelA proteins. Analyses were performed by Clustal Analysis using the Lasergene Multalign program (DNAStar, Madison, WI) with gap and gap-length penalties of 10 and a PAM250 weight table. Residues are boxed and shaded when they show chemical group similarity in 4 out

where homology between plant and bacterial proteins is highest. The plant proteins show two insertions that are not present in the bacterial protein--one, P-CR, is conserved among the plant CelA genes, while a second insertion is hypervariable (HVR) between plant genes. The presence of the P-CR and HVR regions led to inaccurate alignments when the entire proteins were compared; the optimal alignments shown here were thus performed in five separate blocks. Regions U-1 through U-4 are predicted to be critical for UDP-glc binding and catalysis in bacterial CelA proteins; the predicted critical D residues and QXXRW motif are boxed and starred respectively. Potential sites of N-glycosylation are indicated by -G-.

Figure 4. Kyte-Doolittle hydropathy plots of cotton CelA1 aligned with those of two bacterial CelA proteins. Alignments and designations are based upon those noted in Fig. 2. The hydropathy profiles shown were calculated using a window of 7, although a window of 19 was used for predictions of transmembrane helices that are indicated by the arrows.

Figure 5. An *E. coli* expressed GST cotton CelA-1 fusion protein binds the containing U1 through U4 binds UDP-glc *in vitro*. Panel A shows a hypothetical orientation of the cotton CelA1 protein in the plasma membrane and indicates the cytoplasmic region containing the sub-domains U-1 to U-4. GST-fusion constructs for CelA1 fragments spanning the region between the potential transmembrane helices (A through H) were prepared as described in Materials and Methods. The purified and blotted CelA1 fusion protein fragments were tested as described in Materials and Methods for their ability to bind

32^P-UDP-glc (panel B). M refers to the molecular weight markers while CS and E1 to the full-length and deleted GST-CelA1 fusion polypeptides. The left panel shows proteins stained with Coomassie blue while the other three panels show representative autoradiograms under different binding conditions as described in Materials and Methods. Ph, BSA and Ova refer to the molecular weight standards phosphorylase b, bovine serum albumin and ovalbumin respectively.

Figure 6. Nucleic acid sequences to cDNA of CelA1 protein of cotton (*Gossypium hirsutum*).

Figure 7. Nucleic acid sequences to cDNA of CelA2 protein of cotton (*Gossypium hirsutum*), including approximately the last 3' two-thirds of the encoding region.

Figure 8. Genomic nucleic acid sequences of CelA1 protein of cotton (*Gossypium hirsutum*), including approximately 900 bases of the promoter region 5' to the encoding sequences.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the subject invention, novel constructs and methods are described, which may be used provide for transcription of a nucleotide sequence of interest in cells of a plant host, preferentially in cotton fiber cells to produce cotton fiber having an altered color phenotype.

Cotton fiber is a differentiated single epidermal cell of the outer integument of the ovule. It has four distinct growth phases; initiation, elongation (primary cell wall synthesis), secondary cell wall synthesis, and maturation. Initiation of fiber development appears to be triggered by hormones. The primary cell wall is laid down during the elongation phase, lasting up to 25 days postanthesis (DPA). Synthesis of the secondary wall commences prior to the cessation of the elongation phase and continues to approximately 40 DPA, forming a wall of almost pure cellulose.

The constructs for use in such cells may include several forms, depending upon the intended use of the construct. Thus, the constructs include vectors, transcriptional cassettes, expression cassettes and plasmids. The

transcriptional and translational initiation region (also sometimes referred to as a "promoter,"), preferably comprises a transcriptional initiation regulatory region and a translational initiation regulatory region of untranslated 5' sequences, "ribosome binding sites," responsible for binding mRNA to ribosomes and translational initiation. It is preferred that all of the transcriptional and translational functional elements of the initiation control region are

embodiments, the promoter will be modified by the addition of sequences, such as enhancers, or deletions of nonessential and/or undesired sequences. By "obtainable" is intended a promoter having a DNA sequence sufficiently similar to that of a native promoter to provide for the desired specificity of transcription of a DNA sequence of interest. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences.

Cotton fiber transcriptional initiation regions of cellulose synthase are used in cotton fiber modification.

A transcriptional cassette for transcription of a nucleotide sequence of interest in cotton fiber will include in the direction of transcription, the cotton fiber transcriptional initiation region, a DNA sequence of interest, and a transcriptional termination region functional in the plant cell. When the cassette provides for the transcription and translation of a DNA sequence of interest it is considered an expression cassette. One or more introns may be also be present.

Other sequences may also be present, including those encoding transit peptides and secretory leader sequences as desired.

Downstream from, and under the regulatory control of, the cellulose synthase transcriptional/translational initiation control region is a nucleotide sequence of interest which provides for modification of the phenotype of fiber. The nucleotide sequence may be any open reading frame encoding a polypeptide of interest, for example, an enzyme, or a sequence complementary to a genomic sequence, where the genomic sequence may be an open reading frame, an intron, a noncoding

leader sequence, or any other sequence where the complementary sequence inhibits transcription, messenger RNA processing, for example, splicing, or translation. The nucleotide sequences of this invention may be synthetic, naturally derived, or combinations thereof. Depending upon the nature of the DNA sequence of interest, it may be desirable to synthesize the sequence with plant preferred codons. The plant preferred codons may be determined from the codons of highest frequency in the proteins expressed in the largest amount in the particular plant species of interest. Phenotypic modification can be achieved by modulating production either of an endogenous transcription or translation product, for example as to the amount, relative distribution, or the like, or an exogenous transcription or translation product, for example to provide for a novel function or products in a transgenic host cell or tissue. Of particular interest are DNA sequences encoding expression products associated with the development of plant fiber, including genes involved in metabolism of cytokinins, auxins, ethylene, abscissic acid, and the like.

Methods and compositions for modulating cytokinin expression are described in United States Patent No. 5,177,307, which disclosure is hereby incorporated by reference. Alternatively, various genes, from sources including other eukaryotic or prokaryotic cells, including bacteria, such as those from *Agrobacterium tumefaciens* T-DNA auxin and cytokinin biosynthetic gene products, for example, and mammals, for example interferons, may be used.

Alternatively, the present invention provides the sequences to cotton cellulose synthase, which can be expressed, or down regulated by antisense or co-suppression with its own, or other cotton or other fiber promoters to modify fiber phenotyp.

In cotton, primary wall hemicellulose synthesis ceases as secondary wall synthesis initiates in the fiber, and there are only two possible β -glucans synthesized in fibers at the time these genes are highly-expressed; callose and cellulose (20). The following data strongly argue against the plant CelA genes coding for callose synthase: 1) callose synthase binds UDP-glucose to form callose, and 2) callose synthase is inhibited by cellobiose.

and is activated in a Ca^{2+} -dependent manner (2), while the CelA1 polypeptide fragment containing the UDP-glc binding site preferentially binds UDP-glc in a Mg^{2+} -dependent manner, similar to bacterial cellulose synthase (9); 2) the timing 5 of synthesis of callose *in vivo* in developing cotton fiber (20) does not match the expression of the cotton CelA genes (Fig. 1); 3) comparison of the CelA gene sequences with those of suspected 1,3- β -glucan synthase genes from yeast (21)

10 It is still possibille that the CelA protein might encode both activities, as hypothesized some years ago (22-23), and the plant CelAs might be responsible for direct polymerization of glucan from UDP-glc as proposed for *A. xylinum*, although they may catalyze synthesis of a lipid-glc precursor as 15 proposed for the CelA protein of *A. tumefaciens*.

In addition to their similarities, the plant CelA genes show several very interesting divergences from their bacterial ancestors, and these may account for the previous lack of success in using bacterial probes to detect these cDNA clones. 20 However, a BLAST search of protein data banks (24) using the entire protein sequence of cotton CelA1 always shows highest homology with the bacterial cellulose synthases. Of particular interest is the insertion of two unique, plant-specific regions designated P-CR and HVR. These 25 regions are clearly not artifacts of cloning as they are observed in both cotton genes as well as the rice CelA gene. The three plant proteins show a high degree of amino acid homology to each other throughout most of their length, diverging only at the N- and C-terminal ends and the very 30 interesting HVR region. It is tempting to speculate that the HVR region may confer some specificity of function; the highly-charged and cysteine rich nature of the first portion of HVR could make this region a potential candidate for interaction with specific regulatory proteins, for 35 cytoskeletal elements, or for redox regulation. In addition, we note the presence of several cysteine residues near the N- and C-terminal regions of the protein that might serve as

substrates for palmytolylation and also serve to help anchor the protein in the membrane (25).

In summary, the finding of these plant CelA homologs potentially opens up an exciting chapter in research on cellulose synthesis in higher plants. Their finding is of particular significance since biochemical approaches to identification of plant cellulose synthase have proven exceedingly difficult. One obvious challenge will be to gain definitive proof that these genes are truly functional in cellulose synthesis *in vivo*. Other promising goals will be to identify other components of a complex that might interact with CelA, such as that proposed for sucrose synthase (26), and/or a regulatory subunit that binds cyclic-di-GMP (9,27) or other glycosyltransferases (10,11).

Transcriptional cassettes may be used when the transcription of an anti-sense sequence is desired. When the expression of a polypeptide is desired, expression cassettes providing for transcription and translation of the DNA sequence of interest will be used. Various changes are of interest; these changes may include modulation (increase or decrease) of formation of particular saccharides, hormones, enzymes, or other biological parameters. These also include modifying the composition of the final fiber that is changing the ratio and/or amounts of water, solids, fiber or sugars.

Other phenotypic properties of interest for modification include response to stress, organisms, herbicides, brushing, growth regulators, and the like. These results can be achieved by providing for reduction of expression of one or more endogenous products, particularly an enzyme or cofactor, either by producing a transcription product which is complementary (anti-sense) to the transcription product of a native gene, so as to inhibit the maturation and/or expression of the transcription product, or by providing for expression of a gene, either endogenous or exogenous, to be associated with the development of a plant fiber.

The termination region which is employed in the expression cassette will be primarily one of convenience, since the termination regions appear to be relatively

interchangeable. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, may be derived from another source. The termination region may be naturally occurring, or wholly 5 or partially synthetic. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. In some embodiments, it may be desired to use the 3'

10 initiation region used in a particular construct.

As described herein, in some instances additional nucleotide sequences will be present in the constructs to provide for targeting of a particular gene product to specific cellular locations.

15 Similarly, other constitutive promoters may also be useful in certain applications, for example the mas, Mac or DoubleMac, promoters described in United States Patent No. 5,106,739 and by Comai et al., *Plant Mol. Biol.* (1990) 15:373-381). When plants comprising multiple gene constructs are 20 desired, the plants may be obtained by co-transformation with both constructs, or by transformation with individual constructs followed by plant breeding methods to obtain plants expressing both of the desired genes.

25 A variety of techniques are available and known to those skilled in the art for introduction of constructs into a plant cell host. These techniques include transfection with DNA employing *A. tumefaciens* or *A. rhizogenes* as the transfecting agent, protoplast fusion, injection, electroporation, particle acceleration, etc. For 30 transformation with *Agrobacterium*, plasmids can be prepared in *E. coli* which contain DNA homologous with the Ti-plasmid, particularly T-DNA. The plasmid may or may not be capable of replication in *Agrobacterium*, that is, it may or may not have a broad spectrum prokaryotic replication system such as does, 35 for example, pRK290, depending in part upon whether the transcription cassette is to be integrated into the Ti-plasmid or to be retained on an independent plasmid. The *Agrobacterium* host will contain a plasmid having the vir genes

necessary for transfer of the T-DNA to the plant cell and may or may not have the complete T-DNA. At least the right border and frequently both the right and left borders of the T-DNA of the Ti- or Ri-plasmids will be joined as flanking regions to 5 the transcription construct. The use of T-DNA for transformation of plant cells has received extensive study and is amply described in EPA Serial No. 120,516, Hoekema, In: The Binary Plant Vector System Offset-drukkerij Kanters B.V., Albllasserdam, 1985, Chapter V, Knauf, et al., Genetic Analysis 10 of Host Range Expression by *Agrobacterium*, In: Molecular Genetics of the Bacteria-Plant Interaction, Puhler, A. ed., Springer-Verlag, NY, 1983, p. 245, and An, et al., *EMBO J.* (1985) 4:277-284.

For infection, particle acceleration and electroporation, 15 a disarmed Ti-plasmid lacking particularly the tumor genes found in the T-DNA region) may be introduced into the plant cell. By means of a helper plasmid, the construct may be transferred to the *A. tumefaciens* and the resulting transfected organism used for transfecting a plant cell; 20 explants may be cultivated with transformed *A. tumefaciens* or *A. rhizogenes* to allow for transfer of the transcription cassette to the plant cells. Alternatively, to enhance integration into the plant genome, terminal repeats of 25 transposons may be used as borders in conjunction with a transposase. In this situation, expression of the transposase should be inducible, so that once the transcription construct is integrated into the genome, it should be relatively stably integrated. Transgenic plant cells are then placed in an appropriate selective medium for selection of transgenic cells 30 which are then grown to callus, shoots grown and plantlets generated from the shoot by growing in rooting medium.

To confirm the presence of the transgenes in transgenic cells and plants, a Southern blot analysis can be performed using methods known to those skilled in the art. Expression 35 products of the transgenes can be detected in any of a variety of ways, depending upon the nature of the product, and include immune assay, enzyme assay or visual inspection, for example to detect pigment formation in the appropriate plant part or

cells. Once transgenic plants have been obtained, they may be grown to produce fiber having the desired phenotype. The fibers may be harvested, and/or the seed collected. The seed may serve as a source for growing additional plants having the desired characteristics. The terms transgenic plants and transgenic cells include plants and cells derived from either transgenic plants or transgenic cells.

The various sequences provided herein may be used as

10 may be useful in the present invention, for example, to obtain related transcriptional initiation regions from the same or different plant sources. Related transcriptional initiation regions obtainable from the sequences provided in this invention will show at least about 60% homology, and more
15 preferred regions will demonstrate an even greater percentage of homology with the probes.

Of particular importance is the ability to obtain related transcription initiation control regions having the timing and tissue parameters described herein. Thus, by employing the
20 techniques described in this application, and other techniques known in the art (such as Maniatis, et al., *Molecular Cloning, - A Laboratory Manual* (Cold Spring Harbor, New York) 1982), other encoding regions or transcription initiation regions of cellulose synthase as described in this invention
25 may be determined. The constructs can also be used in conjunction with plant regeneration systems to obtain plant cells and plants; thus, the constructs may be used to modify the phenotype of fiber cells, to provide cotton fibers which are colored as the result of genetic engineering to heretofor
30 unavailable hues and/or intensities.

Various varieties and lines of cotton may find use in the described methods. Cultivated cotton species include *Gossypium hirsutum* and *G. babadense* (extra-long staple, or Pima cotton), which evolved in the New World, and the Old
35 World crops *G. herbaceum* and *G. arboreum*.

By using encoding sequences to enzymes which control wood quality and wood product characteristics, i.e., cellulose synthase and O-methyltransferase (a key enzyme in lignin

biosynthesis) the relative synthesis of cellulose and lignin by plants may be controlled. Transformation of the plant genome with a recombinant gene construct which contains the gene specifying an enzyme critical to the synthesis of cellulose or lignin or a lignin precursor, in either a sense or in an antisense orientation. If an antisense orientation, the gene will transcribed so mRNA having a sequence complementary to the equivalent mRNA transcribed from the endogenous gene is expressed, leading to suppression of the synthesis of lignin or cellulose.

If the recombinant gene has the lignin enzyme gene in normal, or "sense" orientation, increased production of the enzyme may occur when the insert is the full length DNA but suppression may occur if only a partial sequence is employed.

Furthermore, the expression of one may be increased in this manner while the other is reduced. For instance, the production of cellulose may be increased through the overexpression of cellulose synthase, while lignin production is reduced. By thus reducing the relative lignin content, the quality of wood for paper production would be improved.

EXAMPLES

The following examples are offered by way of illustration and not by limitation.

25 Example 1
 cDNA libraries

An unamplified cDNA library was used to prepare the Lambda Uni-Zap vector (Stratagene, LaJolla, CA) using cDNA derived from polyA+ mRNA prepared from fibers of *Gossypium hirsutum* Acala SJ-2 harvested at 21 DPA, the time at which secondary wall cellulose synthesis is approaching a maximal rate (13). Approximately 250 plaques were randomly selected from the cDNA library, phages purified and plasmids excised from the phage vector and transformed.

35 The resulting clones/inserts were size screened on 0.8% agarose gels (DNA inserts below 600bp were excluded).

Example 2

Isolation and Sequencing of cDNA Clones

Plasmid DNA inserts were randomly sequenced using an Applied Biosystems (Foster City, CA) Model 373A DNA sequencer. A search of the GenBank EST databank revealed that there were 5 at least 23 rice and 8 *Arabidopsis* EST clones that contain sequences similar to the cotton CelA1 DNA sequence. EST clone S14965 was obtained from Y. Nagamura (Rice Genome Research Program, Tsukuba). A series of deletion mutants were

10 Institute of Science (Renovot).

Example 3Northern and Southern Analyses.

Cotton plants (*G. hirsutum* cv. Coker 130) were grown in 15 the greenhouse and tissues harvested at the appropriate times indicated and frozen in liquid N₂. Total cotton RNA and cotton genomic DNA was prepared and subjected to Northern and Southern analyses as described previously (14).

20

Example 4UDP-Glc Binding Studies

To construct a GST-CelA1 protein fusion, a 1.6kb DNA CelA1 DNA fragment containing a putative cytoplasmic domain between the second and third transmembrane helices was PCR 25 amplified with the primers ATTGAATTCTGGTGTGGATCAGTT and ATTCTCGAGTGAAAGGGATTGAAA in a reaction containing 1 ng plasmid DNA (clone 213) as template. The amplified fragment was unidirectionally cloned into the EcoRI and XhoI sites of the GST expression vector pGEX4T-3 (Pharmacia), generating a 30 fusion protein GST-CS containing the amino acids Ser215 to Leu759 of the cotton CelA1 protein. Two CelA1 gene internal *Pst*I sites within the plasmid pGST-CS were used to generate the deletion mutant pGST-CSΔU1, which lacks 196 amino acids (and the U1 binding region) from Val252 to Ala447.

35 For the UDGP binding assays, α -³²P-labeled UDP-glc was prepared as described (15). The two fusion proteins GST-CS and GST-CSΔU1 were expressed in *E. coli* and purified from inclusion bodies (16). Proteins were suspended in sample

buffer, heated to 100° C for 5 min and approximately 50ng of the two fusion protein products and molecular weight standards (Bio-Rad) subjected to SDS-PAGE using 4.5% and 7.5% acrylamide in the stacking and separating gels, respectively (17). After 5 electrophoresis, protein transfer to nitrocellulose filters was carried out in transfer buffer (25mM Tris, 192mM glycine and 20% (v/v) methanol). The filter was briefly rinsed in deionized H₂O and incubated in PBS buffer for 15 min, then stained with Ponceau-S in PBS buffer. After washing in 10 deionized H₂O, protein was further renatured on the filter by incubation in PBS buffer for 30 min and used directly for binding assays. All binding buffers contained 50mM HEPES/KOH (pH 7.3), 50mM NaCl and 1mMDTT. In addition, binding buffers contained either 5mM MgCl₂ and 5mM EGTA (Buffer Mg/EGTA), 5mM 15 EDTA (Buffer EDTA) or 1mM CaCl₂ and 20mM cellobiose (Buffer Ca/CB). Binding reaction was carried out in 7ml containing 32P-labeled UDP-glc (1x 10⁷ cpm) at room temperature for 3 hours with constant shaking. Filters were washed separately three times in 20ml washing buffer consisting of 50mM 20 HEPES/KOH (pH 7.3) and 50mM NaCl for 5min each, briefly dried and analyzed on a Bio-imaging analyzer BAS1000 (Fugi).

Example 5

Identification, Differential Expression and Genomic Analysis of Cotton CelA Genes

During the course of screening and sequencing random cDNA clones from a cotton fiber specific cDNA library prepared from RNA collected approximately 21 dpa, it was discovered that two 25 cDNA clones that initially exhibited small blocks of amino acid homology to the proteins encoded by the bacterial CelA genes. Clone 213 appeared to be full-length cDNA while another distinct clone, 207, appeared to be a partial clone 30 relative to the length of 213. These two clones were partially homologous at the nucleotide and amino acid levels 35 and designated CelA1 and CelA2 respectively.

These clones were then utilized as probes for Northern blot analysis to determine their differential expression in cotton tissues and developing cotton fiber. Figure 1

indicates the expression pattern for the CelA1 gene. The CelA1 gene encodes a mRNA of approximately 3.2kb in length and is expressed at extremely high levels in developing fiber, beginning at approximately 17 dpa, the time at which secondary wall cellulose synthesis is initiated(13). The gene is also expressed at low levels in all other cotton tissues, most notably in root, flower and developing seeds. Since regions of these genes are somewhat homologous at the nucleotide

10 hypervariable regions described in Fig 3) to distinguish the specific expression patterns of CelA1 and CelA2. These gene specific probes generated expression patterns (data not shown) for the two genes identical to that shown in Figure 1, except that a very low mRNA level was also detected in the primary
15 wall phase of fiber development (5-14dpa) for the CelA2 gene when the blots were overexposed. The CelA2 gene specific probe also encoded a 3.2kb mRNA, analogous in size to the mRNA specified by the gene for CelA1. Messenger RNAs for both genes exhibit a characteristic degradation pattern similar to
20 other mRNAs specifically expressed late in fiber development (J. Pear, unpublished observations) and this degradation is not a result of the integrity of the mRNA preparations (14). We estimate that both cotton CelA genes are expressed in
25 developing fiber approximately 500 times their level of expression in other cotton tissues and that they constitute approximately 1-2% of the 24dpa fiber mRNA.

In order to estimate the number of CelA genes in the cotton genome, Southern analysis was performed utilizing both CelA cDNAs independently as probes (Fig 2). Although the two
30 cotton genes are fairly non-homologous at the nucleotide level over their entire length, there are regions of homology (the H1, H2 and H3 regions described below) and it was thought these regions could be useful in identifying other cotton CelA genes. Figure 2 indicates that the CelA1 cDNA probe will
35 hybridize, albeit weakly, to the CelA2 genomic equivalent and vice versa. The *HindIII* pattern for both genes and cDNA probes is particularly discriminating. There are also a number of other weakly hybridizing bands in these digests and

from these data we estimate that the cotton CelA genes constitute a small family of approximately four genes.

Homology of Plant and Bacterial CelA Gene Products.

In addition to the two similar cotton CelA genes, a homologous cDNA clone was discovered in the dBest databank* of rice and *Arabidopsis* ESTs. Accession No. D48636, the rice clone having the longest insert was obtained and sequenced, and the homology comparisons with bacterial proteins reported here also include results with the rice CelA. Figure 3 shows the results of a multiple alignment of the deduced amino acid sequences from the three plant CelA genes and four bacterial CelA genes from *A. xylinum* (AcsAB and BcsA), *E. coli*, and *A. tumefaciens*. Figure 4 shows hydropathy plots (18) of cotton CelA1 similarly aligned with two bacterial CelA proteins and serves as a more general summary of the overall homologies.

Of the plant genes, only the cotton CelA1 appears to be a full-length clone of 3.2kb exhibiting an open reading frame that could potentially code for a polypeptide of 109,586 kD, a pI of 6.4, and four potential sites of N-glycosylation.

Comparison of the N-terminal region of cotton CelA1 with bacterial genes indicates that the plant protein has an extended N-terminal similar in length and hydropathy profile, but with only poor amino acid sequence homology to the *A. tumefaciens* CelA protein. In general, sequence homology of plant and bacterial genes in both the N-terminal and C-terminal regions is poor. However, although overall similarity comparing plant to bacterial proteins is less than 25%, three homologous regions were identified, called H-1, H-2, and H-3, where the sequence similarity rises to 50-60% at the amino acid level. Interspersed between these regions of homology are two plant-specific regions not found at all in the bacterial proteins. Sequences in the first of these

* The following accession numbers were identified as showing homology with cotton CelA-1. For rice: D48636, D41261, D40691, D46824, D47622, D47175, D41766, D41986, D24655, D23732, D24375, D47732, D47821, D47850, D47494, D24964, D24862, D24860, D24711, D23841, D48053, D48612, D40673; for *Arabidopsis*: T45303, T45414, H76149, H36985, Z30729, H36425, T45311, A35212.

insertions are highly conserved in the plant genes (P-CR), while the second interspersed region seems to be a hypervariable regions (HVR) for there is considerable sequence divergence among the plant proteins analyzed.

5 None of the plant or bacterial CelA proteins contains
obvious signal sequences even though they are presumably
transmembrane proteins (4). However, the overall profiles
suggest two potential transmembrane helices in the N-terminal

10 could anchor the protein in the membrane (see arrows Fig.3 and
also panel A of Fig.5). The amino acid sequence positions for
these predicted transmembrane helices are: A (169-187), B
(200-218), C (759-777), D (783-801), E (819-837), F (870-
888), G (903-921), H (933-951). The central portions of the
15 proteins are more hydrophilic and are predicted to reside in
the cytoplasm and contain the site(s) of catalysis. More
detailed inspection of these hydrophilic stretches reveals
four particularly conserved sub-regions (marked U-1 through
U-4 on Figs. 3-4) that contain the conserved asp (D) residues
20 (in U-1-3) and the motif QXXRW (in U-4) that have been
proposed (12) to be involved in substrate binding and/or
catalysis .

Binding of UDP-glucose. Further evidence that the proteins encoded by these plant genes are CelA homologs comes from our demonstration that a DNA segment encoding the central region of the cotton CelA1 protein, over-expressed in *E. coli*, binds UDP-glc. We subcloned a 1.6 kb fragment of the cotton CelA1 clone to create a hybrid gene that encodes GST fused to the CelA1 sequence encoding amino acid residues 215-759 of the CelA1 protein (Fig. 5a). This region spans U-1 through U-4 that are suspected to be critical for UDP-glc binding. As a control, another GST fusion was created using a 1.0 kb *Pst*I fragment that had the U-1 region deleted and might not be predicted to bind UDP-glc. The fusion proteins were overexpressed in *E. coli*, purified, and shown to have the predicted sizes of approximately 87 and 64 kD, respectively (Fig. 5b). The purified proteins were then subjected to SDS-PAGE, and blotted to nitrocellulose. Blotted proteins

were renatured, and incubated with ^{32}P -UDP-glc in order to test for binding (Fig. 5b). As predicted, the 87 kD GST-CelA1 fusion does indeed bind UDP-glc in a Mg^{2+} dependent manner, while the shorter fusion with the U-1 domain deleted did not show any binding (Although not observed in the experiment shown, in some experiments very weak labeling in the presence of Ca^{2+} could be observed). As further controls, note that the molecular weight standards BSA and ovalbumin, proteins lacking UDP-glc binding sites, show no interaction with UDP-glc, while phosphorylase b, an enzyme inhibited by UDP-glc (19), binds this substrate.

Figure 6 provides the encoding sequence to the cDNA to celA1 (start ATG at ~ base 179), while Figure 7 provides the encoding sequence to the approximately two-thirds 3' of the cDNA to celA2.

Example 6

Genomic DNA

cDNA for the cellulose synthase clones was used to probe 20 for genomic clones. For both, full length genomic DNA was obtained from a library made using the lambda dash 2 vector from Stratagene®, which was used to construct a genomic DNA library from cotton variety Coker 130 (*Gossypium hirsutum* cv. coker 130), using DNA obtained from germinating seedlings.

The cotton genomic library was probed with a cellulose synthase probe and genomic phage candidates were identified and purified. Figure 8 provides an approximately 1 kb sequence of the cellulose synthase promoter region which is immediately 5' to the celA1 encoding region. The start of the 30 cellulose synthase enzyme encoding region is at the ATG at base number 954.

Example 7

Cotton Transformation

Explant Preparation

Promoter constructs comprising the cellulose synthase promoter sequences of celA1 can be cotton prepared. Coker 315 seeds are surface disinfected by placing in 50% Clorox (2.5%

sodium hypochlorite solution) for 20 minutes and rinsing 3 times in sterile distilled water. Following surface sterilization, seeds are germinated in 25 x 150 sterile tubes containing 25 mls 1/2 x MS salts: 1/2 x B5 vitamins: 1.5% glucose: 0.3% gelrite. Seedlings are germinated in the dark at 28°C for 7 days. On the seventh day seedlings are placed in the light at 28±2°C.

10 Single colonies of *A. tumefaciens* strain 2760 containing binary plasmids pCGN2917 and pCGN2926 are transferred to 5 ml of MG/L broth and grown overnight at 30°C. Bacteria cultures are diluted to 1 x 10⁸ cells/ml with MG/L just prior to cocultivation. Hypocotyls are excised from eight day old 15 seedlings, cut into 0.5-0.7 cm sections and placed onto tobacco feeder plates (Horsch et al. 1985). Feeder plates are prepared one day before use by plating 1.0 ml tobacco suspension culture onto a petri plate containing Callus Initiation Medium CIM without antibiotics (MS salts: B5 20 vitamins: 3 % glucose: 0.1 mg/L 2,4-D: 0.1 mg/L kinetin: 0.3% gelrite, pH adjusted to 5.8 prior to autoclaving). A sterile filter paper disc (Whatman #1) was placed on top of the feeder cells prior to use. After all sections are prepared, each section was dipped into an *A. tumefaciens* culture, blotted on 25 sterile paper towels and returned to the tobacco feeder plates.

Following two days of cocultivation on the feeder plates, hypocotyl sections are placed on fresh Callus Initiation Medium containing 75 mg/L kanamycin and 500 mg/L 30 carbenicillin. Tissue is incubated at 28±2°C, 30uE 16:8 light:dark period for 4 weeks. At four weeks the entire explant is transferred to fresh callus initiation medium containing antibiotics. After two weeks on the second pass, the callus is removed from the explants and split between 35 Callus Initiation Medium and Regeneration Medium (MS salts: 40mM KNO₃: 10 mM NH₄Cl:B5 vitamins:3% glucose:0.3% gelrite:400 mg/L carb:75 mg/L kanamycin).

Embryogenic callus is identified 2-6 months following initiation and was subcultured onto fresh regeneration medium. Embryos are selected for germination, placed in static liquid Embryo Pulsing Medium (Stewart and Hsu medium: 0.01 mg/l NAA: 5 0.01 mg/L kinetin: 0.2 mg/L GA3) and incubated overnight at 30°C. The embryos are blotted on paper towels and placed into Magenta boxes containing 40 mls of Stewart and Hsu medium solidified with Gelrite. Germinating embryos are maintained at 28±2°C 50 uE m⁻²s⁻¹ 16:8 photoperiod. Rooted plantlets are 10 transferred to soil and established in the greenhouse.

Cotton growth conditions in growth chambers are as follows: 16 hour photoperiod, temperature of approximately 80-85°, light intensity of approximately 500μEinstins. Cotton growth conditions in greenhouses are as follows: 14-16 hour 15 photoperiod with light intensity of at least 400μEinstins, day temperature 90-95°F, night temperature 70-75°F, relative humidity to approximately 80%.

Plant Analysis

20 Flowers from greenhouse grown T1 plants are tagged at anthesis in the greenhouse. Squares (cotton flower buds), flowers, bolls etc. are harvested from these plants at various stages of development and assayed for observable phenotype or tested for enzyme activity.

25

Example 7 Transformation of Tree Species

30 Numerous methods are known to the art for transforming forest tree species, for example U.S. Patent No. 5,654,190 discloses a process for producing transgenic plant belonging to the genus *Populus*, the section *Leuce*.

35 The above results demonstrate how the cellulose synthase cDNA may be used to alter the phenotype of a transgenic plant cell, and how the promoter may be used to modify transgenic cotton fiber cells.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application are specifically 5 and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail, by way of illustration and example for purposes of clarity and understanding, it will be readily apparent to

10 modifications may be made thereto, without departing from the spirit or scope of the appended claims.

CLAIMS

What is claimed is:

1. An isolated DNA encoding sequence to a plant cellulose synthesis enzyme.
- 5 2. The DNA encoding sequence of Claim 1 wherein said cellulose synthesis enzyme is cellulose synthase.
3. The DNA encoding sequence of Claim 2 wherein said cellulose synthase is from cotton.
- 10 4. The DNA encoding sequence of Claim 3 wherein said cotton cellulose synthase is celA1.
5. The DNA encoding sequence of Claim 4 wherein said celA1 is encoded by the sequence of Figure 6.
- 15 6. The DNA encoding sequence of Claim 3 wherein said cotton cellulose synthase is celA2.
7. The DNA encoding sequence of Claim 6 wherein said celA2 is encoded by the sequence of Figure 7.
8. An isolated DNA encoding sequence to a plant cellulose synthesis promoter region.
- 20 9. The promoter encoding sequence of Claim 8 wherein said cellulose synthesis promoter region is to cellulose synthase.
10. The promoter sequence of Claim 9 wherein said cellulose synthase promoter region is from cotton.
- 25 11. The promoter sequence of Claim 10 wherein said cotton cellulose synthase promoter region is from celA1.
12. The promoter sequence of Claim 11 wherein said cotton cellulose synthase promoter region is the from sequence of Figure 8.
- 30 13. A recombinant DNA construct comprising any of the DNA encoding sequences of Claims 1-10.
14. The DNA construct of Claim 13 comprising as operably joined components in the direction of transcription, a cotton fiber transcriptional factor and the sequence of any of Claims 1-7.
- 35 15. A plant cell comprising a DNA construct of Claims 13 or 14.
16. A plant comprising a cell of Claim 15.

17. A method of modifying fiber phenotype in a cotton plant, said method comprising:

transforming a plant cell with DNA comprising a construct of Claims 13 or 14.

5 18. A method of modifying the wood quality phenotype in a forest tree species, said method comprising:

transforming a plant cell of said species with

10 19. A method according to Claim 18 wherein said cellulose synthesis enzyme is cellulose synthase and wherein the encoding sequence is in an antisense orientation, wherein transcribed mRNA from said sequence is complementary to the equivalent mRNA transcribed from 15 the endogenous gene, whereby the synthesis of cellulose in said plant cell is suppressed.

20 20. A method according to Claim 18, wherein said cellulose synthesis enzyme is cellulose synthase and wherein the encoding sequence is in a sense orientation, and wherein the synthesis of cellulose in said plant cell is increased.

25 21. A method according to Claim 20 wherein said plant cell additionally comprises a construct encoding a sequence to an enzyme involved in the synthesis of lignin or a lignin precursor.

30 22. A method according to Claim 20 wherein said lignin encoding sequence is in an antisense orientation, wherein transcribed mRNA from said sequence is complementary to the equivalent mRNA transcribed from the endogenous gene, whereby the synthesis of lignin is suppressed.

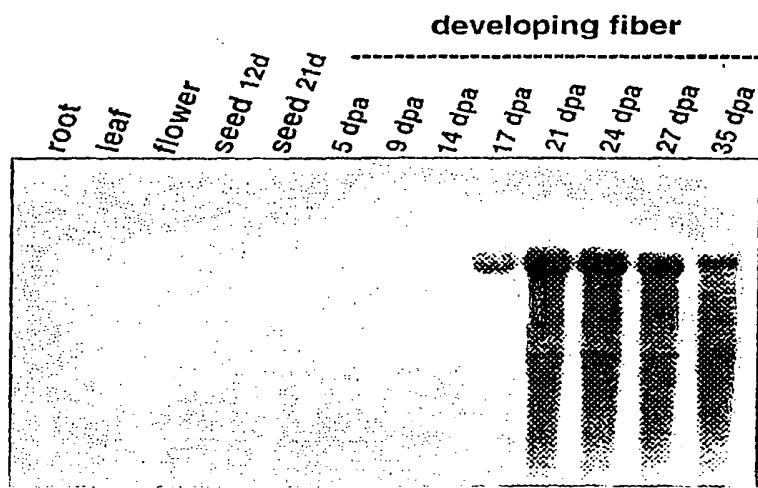


FIG. 3

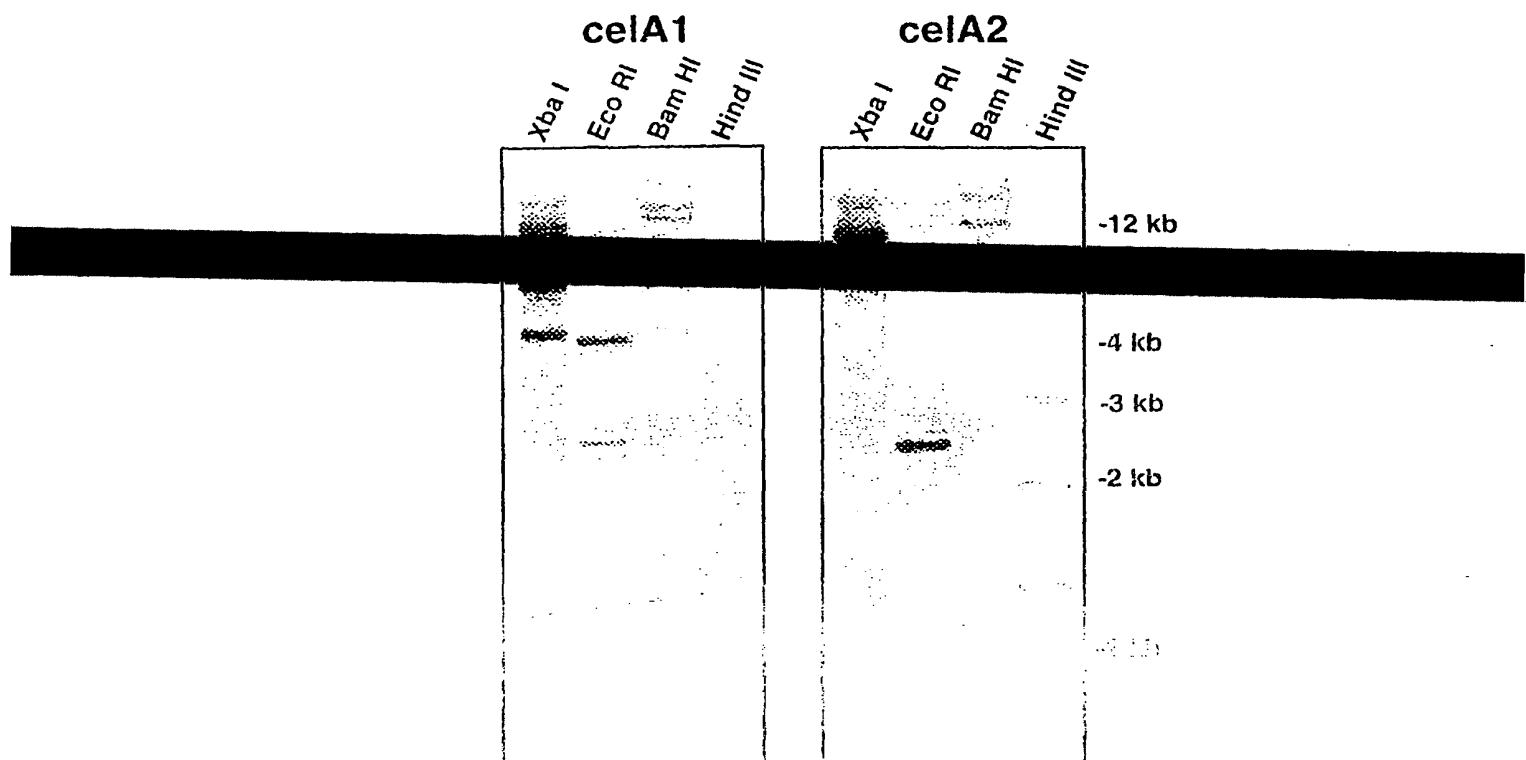


FIG. 2

2/18

SUBSTITUTE SHEET (RULE 26)

G HIRUTUM CELA-1 | MME S G V - P V C H T C G C H V G L M V N G Z P F V A C H E - C M F P I C K S C F F Y D L K E R G K A C L R
G HIRUTUM CELA-2 |
O SALVA CELA |
A KHMUM ACSAI |
E COLI ORF f692 |
TUNEFACIENS CELA | M C R C G R A V R S R P V C R P - G O L V V R A S P R P R S R N H S C R P - P L R L S F P P R H R V R H C O R D L A W E P C R M I A V R N K A A R S H R R R P R C

H-2 U-2 G

422	V SR E K R P C Y Q H H K K A G A E N A L V O V S A V L T H A R P I N L O C D M Y H N S K A V R E A M C F L M D P O V G R D V C Y V O P O R E	125	V SR E K R P C Y Q H H K K A G A E N A L V R U V S A V L T H A R P I N L O C D M Y H N S K A H R E A M C F L M D P O F G K K L C Y V O P O R E	325	V S R E K A P C F O H H K K A G A M H V R U V S A V L T H G O Y M L N L D C M Y H N S K A L R E A M C F L M D P N L G R S V C Y V O P O R E	207	I A R P T N . . . E H A K A G N L N Y A M I G H . . . T U G D Y V I L I F D C D H . . . V P T R A F L O L T H G M H V E . . . D R X I A L M O T P H H F	151	I A R T T H . . . E H A K A G N I N N A L K Y . . . A K G E F V S I F D C D H . . . V P T R A S F L O M T H G M F L K . . . E N O L A M H O T P H H F	316	L T R E B N . . . V H A K A G N L N G L A H . . . S T E E L V Y T V D A H . . . A P A R D E P L I E T Y G M F D E . . . D P R L F L V Y Q T P M F E
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511 FFDINMKGIDGIVYVGTGCVFNRQALYGYGPSPMSYPKSS---SSSCSCCCCPG-KKEPKDPS
 5214 FFDINMLGLDGIVYVGTGCVFNRQALYGYDPVSEKRPKMTDCWMPSWCCCCGGSRKSKKKGEEKKGLGG
 5414 FFDINLHGLDGIVYVGTGCVFNRQALYGYEPPIOKKK-----GSFLSSSLCGGAKKASKSK-KKSK--
 291 FGYGVQDGNDDEHDATFFCGSCAILRRTAI-----
 291 FGYGVQDGNDDFWDATFFCGSCAILRNEAJ-----
 2235 FYGLVQDGNDMHDATFFCGSCAVIRRKPI-----
 420 FYGJ1QRLDKWNGAFFFCSAAVRRREAL

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404	I K H M I R G M K S V Y C V P K R P A F K G S A P I N L S D R I H C V I R W A L S G S V E I F L S R H C P L W Y G G - M K K W L E R A Y I N T I
504	F K M H A R C W R S I Y C H P K R P A F K G S A P I N L S D R I H C V I R W A L S G S V E I F L S R H C P L W Y G G - M K K W L E R A Y I N T I
505	S U G - L K H O R L G S T A Y - L R I P L A G G L A T E R L I L H G D O R V A R W A G H G L Q I F R I D N - P L - - E G R G [L S N G O R L C Y L I S A M
506	J J 3 9 L K H O R L G S T A Y - L R I P L A G G L A T E R L I L H G D O R V A R W A G H G L Q I F R I D N - P L - - E G R G [L S N G O R L C Y L I S A M
507	J J 3 9 L R M O R G N S T A Y - L R I P V A G G L A T E R L I L H G D O R V A R W A G H G L Q I F R I D N - P L - - E G R G [L S N G O R L C Y L I S A M
508	202 L R M O R G N S T A Y - L R I P V A G G L A T E R L I L H G D O R V A R W A G H G L Q I F R I D N - P L - - E G R G [L S N G O R L C Y L I S A M
509	L R M O R G N S T A Y - L R I P V A G G L A T E R L I L H G D O R V A R W A G H G L Q I F R I D N - P L - - E G R G [L S N G O R L C Y L I S A M
510	167 L A L H S R G M N S V Y - V D K P L I A G L O E A T F A S H I G O N S R A W O G H M Q I I - F R O - P L - - E F R G [L S N G O R L C Y L I S A M

FIG. 3B

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7773	C K F I P T L S H M A N S V L F L G F I S I V T A V L E I A M S G V S I E D L W R N E O F W V - I G G V S A H L F A V F Q G F L K M [REDACTED]	T U T A K A D - D A G F C E L -	
499	C K F I P T L S M N L T S V W F L A L F L S I A T C V L E I A M S G V S I O D M W R N E O F W V - I G G V S A H L F A V F Q G F L K M [REDACTED]	T U T A K A D - D T E F G E L -	
681	G K F I P T L S M N L T S V W F L A L F L S I A T C V L E I A M S G V S I O D M W R N E O F W V - I G G V S A H L F A V F Q G F L K M [REDACTED]	T U T A K A D - D E D D P A E L -	
4227	G O N I A R I S P L A L L A Y A I P H M - F - H A V G - T A S K I N K G W R Y S - F W S E V Y E T T H A L F L V R V T I V T L S P S R G F E N V T O K Q G L I E K G H F D I G A V Y	V C V V A G F S U R L N K G Y E -	
4227	G O N I A R I S P L A L L A Y A I P H M - F - H A V G - T A S K I N K G W R Y S - F W S E V Y E T T H A L F L V R V T I V T L S P S R G F E N V T O K Q G L I E K G H F D I G A V Y	V C V V A G F S U R L N K G Y E -	
471	G U N I A R I A S C L A N V L A Y A I P H M - F S H S I A - T A N X V N K G W R Y S - F W S E V Y E T T H A L F L V R V T I V T L S P S R G F E N V T O K Q G L I E K G H F D I G A V Y	V C V V A G F S U R L N K G Y E -	
556	O L G I F V A - S G C E F L A M T A Y M - L Y N - H O N Y L Y G S F R W P - W I S E L Y E V O T V H L L P A V V S V I L -	V C V V A G F S U R L N K G Y E -	
666	W T - - T L L I P P T T L L I V - N M -	[REDACTED]	
509	W T - - T L L I P P T T L L I V - N M -	[REDACTED]	
772	W T - - T L L I P P T T L L I V - N M -	[REDACTED]	
514	P N I L C L I H F G G L A R G V Y E L S I F - G H D O I A E R A Y L L N S A W A M S L I L L A Y A V G R E T Q K B R N S H R I P A T I P V E V A M A D C S -	[REDACTED]	
514	P N I I F A C I H T L C L L I C L F E L T H F N Q L A G I A K R A Y L L N C I N A M I S L I L L A Y A V G R E T Q K B R N S H R I P A T I P V E V A M A D C S -	[REDACTED]	
458	P Y I F L V L L N L V C V A V C I M - R I F Y G C P T E H L - T V V V S M H V F Y N L I V L G G A V A Y S V E S K O V R R S H R V E M T H P A I A R E D G -	[REDACTED]	
642	E F F V I F A L L Y A M A F A V M R I - - Y S E - - P Y K A O V T L V C G M N L N L [REDACTED] G A L G V V Y S E R G D K S A S R I J	[REDACTED]	
899	A W C I P L F -	[REDACTED]	
622	S W C P L F -	[REDACTED]	
808	S W C P L F -	[REDACTED]	
601	E U L S H G C A A V K M - S M P A K L S G P T P V Y I R T V L D G E L - I P A R I T R A G N C R G I F E - D I P A T H L R C K N G K A V E T -	[REDACTED]	
610	D O V S H G C A V V H M - P M P D W S T G P V K T R I H A V L O G E E L - I P A R I T R A G N C R G I F E - D I P A T H L R C K N G K A V E T -	[REDACTED]	
542	Q D F S U C G L G I K I - N G O A Q I L E G Q K V N L L K R G O E Y - V F P T Q V A R V M G C N E V G L K - - L M P U T I T O Q H I D E V O C T P A R A B D T M A L W O D S Y P E D K P L E	[REDACTED]	
7226	D N V S V I N G L L I N I F U S A T H I E K G A T A L I V K V K P H S E Q V P E T M H P L N V V A T V R E G E F V S I G C T E S P Q R A V D O H R L I N D L I P A N S E O W	[REDACTED]	
936	V L W S V L A S V F S I V W -	V R I N P F Y S T A D S T T V S - - - - -	974
662	V L W S V L A S V F S I V W -	V R I N P F L P K Q T G P V L - - - - -	697
685	V L W S V L A S V F S I V W -	V R I N P F L P T A V T G P U T - - - - -	681
690	A N J P H G - H G S O Q H Q C P V P F K W -	R - Y P S Q O F P H O A F C H Q C P V	723
631	L S I K A U F P N K G K M H A N S - R P K M P L A L P V E R -	R E P T I I O S C Q T O E G K I S R A - A S	754
631	L S I K A U F P N K G K M H A N S - R P K M P L A L P V E R -	F I P P R P E R S E T A Q P S D O A L A O O	692
660	G F R G Y R H A E P A S S V K G I F R V L T S L V S M V V S F I P P R P E R S E T A Q P S D O A L A O O	L V K A R R P A P K S A K P V G A U K	860

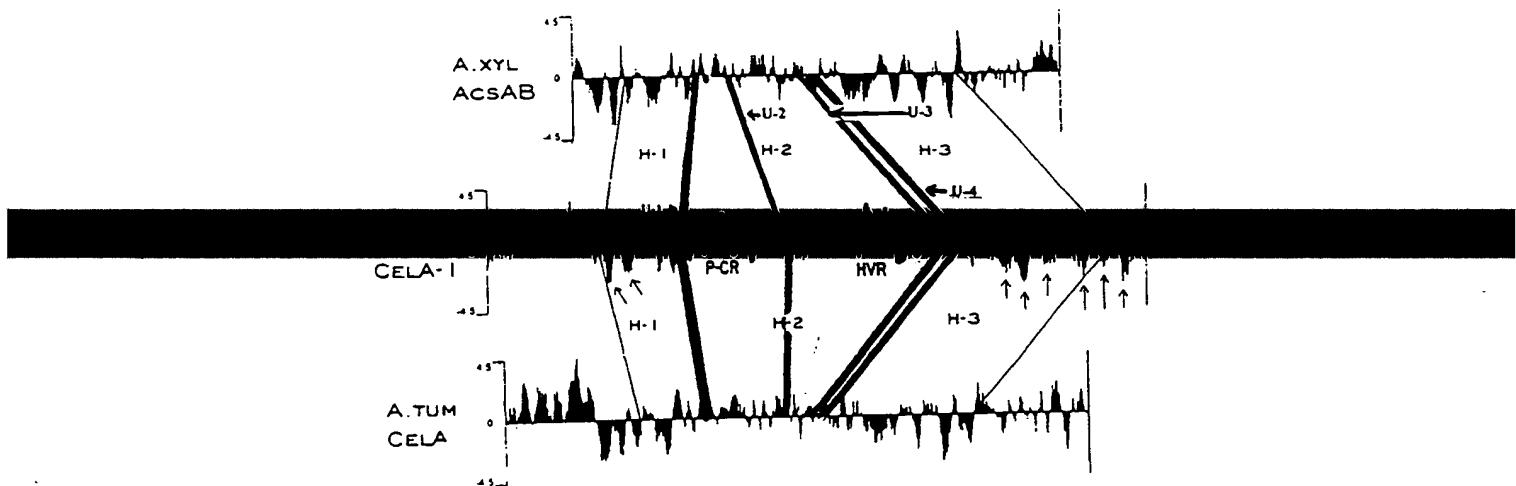


FIG. 4

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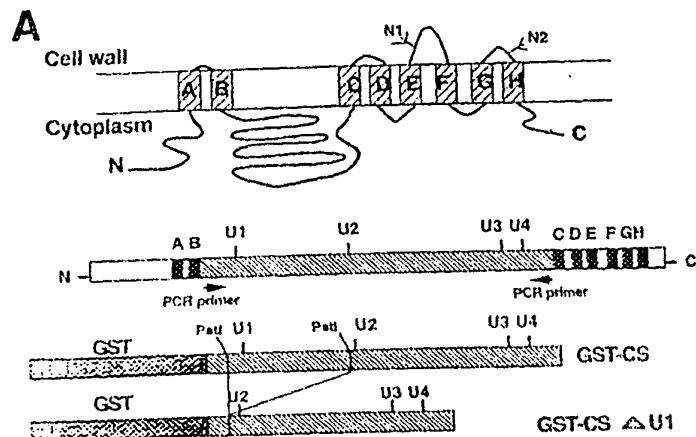


FIG. 5.A

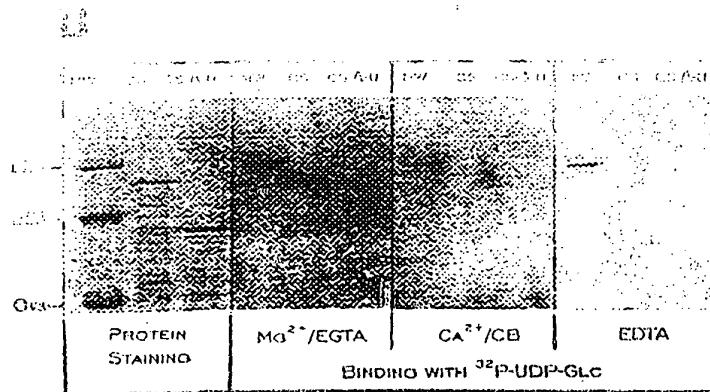


FIG. 5.B

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FIGURE 6A

1800

AACAAACCCCGTTGACAGTGCTTTGGACTGTGGCTCACTTCAGTCATAT

GTGAAACCTGGTTGCATTTCCTGGGTGTTGGATCAGTTCCCTAAGTGG

>HpaI

900

TATCCTTTAACAGGGAAACATAACATTGACAGACTATCTGCCAGATATGA

>PstI

1000

AAGAGAGGGTGAACCTGATGAACTTGCTGCAGTTGACTTCTTCTGAGTA

>BamHI

CAGTGGATCCATTGAAAAGAGGCTCCATTGATTACTGCCAATACGTGCTT

TCCAGCTTCCCTTGGACTACCCGGTGGATAAGGTCTCTTGTATATAC

1100

TGATGATGGTGGGGCCATGCTGACATTGAAATCTCTAGTAGAAGGAGCCG

ACTTTGAAAGAAAGGGTTCCATTCTGCAAAAAATTTCATTGAAACCC

>SmaI

1200

CGGGCACCTGAGTTTACTTCTCACAGAAGATTGATTACTTGAAAGACAA

AGTCCAGCCCTCTTTGAAAGAACGCTAGAGCTATGAAAAGAGATTATG

1300

AAGAGTACAAATTGAAATCAATGCTTTAGTTGCAAAGGCTAGAAACA

>MscI

1400

CCTGATGAAAGGATGACAAATGCAAGATGGAACTTCTGGCCAGGAAACAA

>BclI

1500

CCCCCGTGAATCCCCTGGCATGATTGAGTTTCCCTGGATATAGTGGTG

>XbaI

CTCGTACATGAAAGGAAATGAACTTCTGACTGGTTACGTCTCTAGA

SAGAAGAGACCTGGCTACCAACACCACAAAAAGGCTGGTCTGAAATGC

>PstI

FIGURE 6B

TTTGGTTAGGGTGCTGCAAGTTCTTACAAATGCTCCCTTCATCCTCAATC
 >HpaI
 |
 | 1600
 TTGATTGTGACCCTATGTTAACAAATGCAAGGCAGTAGGGAGGCAATG
 TGCTTCTTGTGGACCCACAAGTTGGTGGATGTATGCTATGTGCAAGTT
 >ClaI
 |
 | 1700
 [REDACTED]

>HpaI
 |
 ACACAGTTTCTTGTGTTAACATGAAAGGTCTTGATGGAATCCAGGG
 1800
 CCAGTTTATGTGGAAACAGGTTGTCTTCAATAGGCAAGCAGTTATGG
 CTATGGTCCACCTTCATGCCAAACTTTCCAGTCACTCTCTCTCTT
 >SmaI
 |
 | 1900
 GCTCTTGTGCGGGGGCAAGAAGGAACTAAAGATCCATCAGAGCTT
 TACAGGGGTGCGGAAACGGGAGAAACTTGTGCTGCCATCTTACCTTAG
 2000
 GGAAATTGACATTTAGATGAGTATGAAAGATCAATGTTGATCTCTCAA
 >HindIII
 |
 CAAGCTTGAAGTAACTTTGGCTTACCTGAGTCCTCAATGAAATCAA
 2100
 CTAATGGAGAAATGGAGGAGTGGCTGAACTGCCAACCCCTCCACACTAA
 CAAGGAAGCAATTGATGTGATCAGCTGGCTATGAAGAGAAAGACTGCAT
 >EcoRS
 |
 | 2200
 | *
 GGGGGAAAGAGATTGGATGGATATACTGTTGAGTCACTGAGGGATATCTTA
 >ClaI >SphI
 | |
 ACCGGCTTCAAAATGCACTGCCGAGGATGGAGATCGATTTACTGCATGCC
 2300
 CTTAAGGCCAGCATTCAAAGGATCTCACCCATCAATCTGTCTGATCGGT

FIGURE 6C

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TGCACCCAGGTTCTCGATGGCTCTTGAATCTGTGAAATTTCCTAAGC
 2400
 AGGCATTGCCCTCTATGGTATGGCTTTGGAGGTGGTCGTCTTAATGGCT
 TCAAAGACTAGCATATATAAACACCATTGTCTATCCTTCACATCCCTC
 2500
 CACTCATTGCCTATTGTTCACTACCAGCCTCTGTCTCACAGGAA
 TTTATCATAACCAACGCTCTCAAACCTGGCAAGTGTCTTTCTTGGCCT
 >XbaI >SacI
 | |
 | |
 | |
 TTTCCCTTCCATTATCGTACTGCTGCTCGAGCTCCGATGGAGTGGTG
 TCAGCATTGAGGACTTATGGCGTAACGAGCAGTTTGGGTATCGGTGGC
 2700
 GTTTCAGCCGAGCTCTTGCCTCTTCAAAGCTTCCATTAGATGCTTGC
 GGGCATTGACACCAACTTTACTGTCACTGCCAAGCAGCTGATGATGCCAG
 >SacI
 |
 |
 |
 ATTTTGGTGAGCTCTACATTGTGAAATGGACTACACTTCTAACTCCCTCCA
 ACACACACTCTCTACATGGTTGGTCTCTTGCCTGGGATTCTCCGA
 >HindIII
 |
 |
 |
 TGCCCTCAACAAAGGGTACGAAGCTTGGGGACCACTCTTGGCAAGCT
 TCTTTTCCCTGGGTCTCCTCCATCTTATCCATTCTCAAAGGTCTT
 3000
 ATGGGACGCCAAAACAGGACACCAACCATTGTCTTGGTCAACCGTTCTCA
 GTTGCCTCTGCTCTCTCTTGTCTTGGTCTGGATCAACCGTTCTCA
 3100
 GCACCGCCGATAGCACCACCGTGTACAGAGCTGCATTCCATTGATTGT
 TGATGATATTATGTCTTAGAATTGAAATCATTGCAAGTAAGTGGAC
 3200
 TGAAACATGCTATTGACTAAGTTTGAAACAGTTGTACCCATTTCATTG
 TTAGCAGTGTAACTTCTAAACAATGCTATGAACTATACATATTCA

FIGURE 6D

>PstI
|
|
| 3300
TTGATATTACATTAATGAAACTACATCAGTCTGCAGAAAAAAAAA
>XbaI >ApaI
| |
AAAAAAAACTCGAGGGGGGGCCCGGTAA

FIGURE 6E

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SUBSTITUTE SHEET (RULE 26)

FIGURE 7A

580 600 620

AAGAAGCTTGTATGTTCAATTCCACAGAGATTTGATGGTATTGATCGTCATGATCGATATGCTAAAC
TTCTCGAAAACAATACAAGTAAAGGTGCTCTAAACTACCATAACTAGCAGTACTAGCTATACGATTAG

>EcoR5

640 660 680 700

GAAATGTTGCTTCTTGATATCAACATGTTGGGATTAGATGGACTCAAGGCCCTGTATATGTAAGGCAC
CTTTACAACAGAAGAAACTATAGTTGACACCCTAACCTGAAAGTCCGGGACATATACATCCGTG

>AlwN1

720

AGGGTGTGTTTCAACAGGCAGGCATTGTATGGCTACGATCCACCAGTCTGAGAAACGACCAAAGATG
TCCCACACAAAAGTTGTCGTCGTAACATACCGATGCTAGGTGGTCAGAGACTTTGCTGGTTCTAC

780 800 820 840

ACATGTGATTGCTGGCCTTCTGGTGTGTTGCGGGAGGTTCTAGGAAGAAATCAAAGAAGAAAG
TGTACACTAACGACCGGAAGAACCAACGACAACAGCCTCCAAGATCCTCTTAGTTCTTCTTC

860 880 900

GTGAAAAGAAGGGCTTACTCGGAGGTCTTTATACGGAAAAAAGAAGAAGATGATGGGCAAAACTATGT
CACTTTCTTCCCGAATGAGCTCCAGAAAATATGCCTTTCTTCTACTACCCGTTTTGATACA

920 940 960 980

GAAAAAAAGGTCTGCACCAGTCTTGATCTGAAGAAATCGAAGAAGGGCTTGAAGGATACGAAGAATTG
CTTTTCCCAGACGTGGTCAGAAACTAGAGCTTCTTAGCTTCTCCGAACTCCATGCTTCTTAAC

>Ase1 >Xmn1 >Xmn1

| | |

1000 1020 1040

* * *

GAGAAATCGACATTAATGTCGAGAAGAATTGAGAAACGATTGGACAATCACCGGTTTCATTGCC
CTCTTAGCTGTAATTACAGCGTCTTCTAAAGCTCTGCTAACGCTGTTAGTGGCAAAAGTAACGGA

>Xmn1

1060 1080 1100 1120

* * *

CAACTTGATGGAAAATGGTGGCCTTCCTGAAGGAACATAATTCCACATCACTGATTAAAGAGGCCATTCA
GTTGAAACTACCTTACCAACCGGAAGGACTTCCTGATTAAGGTGAGTGACTAATTCTCCGGTAAGT

1140 1160 1180

* * *

CGTAATTAGCTGGTTATGAAGAAAAACTGAGTGGGCAAAGAGATCGGATGGATTTATGGGTCGGTG
GCATTAATCGACACCAATACTCTTTGACTCACCCGTTCTAGCCTACCTAAACACATGGCTTT

>Nsi1

1200 1220 1240 1260

* * *

ACGGAAGATATATAACAGGTTCAAGATGCATTGTAGAGGGTGGAAATCGGTTATTGTGTACCGAAAA
TGCCTCTATATAATTGTCCTAAAGTTCTACGTAACATCTCCACCTTAGCCAAATAACACATGGCTTT

1280 1300 1320

FIGURE 7B

GACCGGGATTCAAAGGGTCCGCTCCAATCAATCTCTGGATCGGTGACCAAGTTTGAGATGGGACT
CTGGCCGTAAGTTCCCAGGCAGGTTAGTAGAGAGCCTAGCCAACGTGGTCAAAACCTACCCGTGA

1340 1360 1380 1400

TGGTTCTGTAGAAATTTCCTTAGTCGTCACTGTCCACTTGGTATGGTTATGGTGGAAAAGTGAATGG
ACCAAGACATCTTAAAAGGAATCAGCAGTGACAGGTGAAACCATAACCAATACCACCTTTGACTTTAC

>Aval

>PaeR7I

>XbaI

1420 1440 1460

CTCGAGAGGCTTGCTTATATCAACACCATTGTTACCCCTTCACCTCGATCCCTTACTCGCTATTGTA
GAGCTCTCCGAACGAATATAGTTGTTAACAAATGGAAAGTGGAGCTAGGGAAATGAGCGGATAACAT

>Pvu2

1480 1500 1520 1540

CTATTCCAGCTGTTGTCTTCTCACCGGAAATTCATCATTCAACTCTAAAGCAACCTTACAAGTGTGTG
GATAAGGTGACAACAGAAGAGTGGCGTTAAGTAGTAAGGTGAGATTGTTGAATGTTCACACAC

1560 1580 1600

GTTCTTGGCACTTTCTCCATCATTGCAACTGGAGTGCTTGAACCTCGATGGAGCGGGGTTAGCATC
CAAGAACCGTGAAGGAGAGGTAGTAACGTTGACCTCACGAACTGAAGCTACCTCGCCCCAATCGTAG

1620 1640 1660 1680

CAAGACTGGTGGCGAATGAACAATTCTGGGTGATCGGAGGTGTCCTCCGCCATCTTGTGTCTTCC
GTTCTGACCAACCGCGTTACTTGTAAAGACCCACTAGCCTCACAGAGGCGGGTAGAAAAACGACAGAAGG

1700 1720 1740

AGGGCCTCTCAAAGTCTAGCTGGAGTAGACACCAACTCACCGTAACAGCAAAAGCAGCAGACGATAC
TCCCGGAGGAGTTCAAGGATCGACCTCATGTGGTGAAGTGGCATTGTCGTTCTGCTATG

>EcoRI

1760 1780 1800 1820

AGAATTGGTGAACCTTATCTCTCAAATGGACAACCTCTTAATCCCTCCCACAACCTGATAATACTG
TCTTAAGCCACTTGAATAGAGAAGTTACCTGTTGAGAGAATTAGGGAGGGTGTGAGACTATTATGAC

1840 1860 1880

AACATGGTCGGAGTCGTGGCCGGAGTTCAAGACGCAATCAACAAACGGCTATGGTTCATGGGGTCCATTGT
TTGTACCGCCTCAGCACCGGCTCAAAGTCTGCGTTAGTTGTCGATACCAAGTACCCAGGTAACA

1900 1920 1940 1960

TCGGCAAACGTGTTCTCGCATTCTGGTCATTCTCATCTTACCCATTCTCAAAGGTTGATGGGGAG
AGCCGTTGACAAGAAGCGTAAGACCCAGTAAGAAGTAGAAATGGTAAGGAGTTCCAACCTACCCCTC

>ClaI

1980 2000 2020

FIGURE 7C

ACAAAAACAGGACCCCCACCATTGGTGTGCTTGTCATACTTTGGCATCGATTTCTCACTGGTTGG
TGTGTTGTCCTGCAGGTGGTAACAAACAGAAACCCAGGTATGAAAAGCTAGCTAAAAGAGTGACCAAAC

>ClaI

2040

2060

2080

2100

GTACGGATCGATCCCTTCTGCCAACAAACAGGTCCAGTTCTAACAAATGTGGGTGGAGTGCTAAA
CATGCCTAGCTAGGGAAAGAACGGGTTGTTGTCAGGTCAAGAATTGTTACACCCACCTCACGATT

2120

2140

2160

[REDACTED] TGGTGGTTTACAAAACCTTTCTTATTATTTATTTCCTTTGCCACTACTGTTGATTGCTGTGATTC

2180

2200

2220

2240

TAAAAGGGATTATCTTGTGTAAGTCTCTATGATTGTTGGTCAATTAAATTCTATATGGT
ATTTCCCTAAATAGAACAAACATTTCAGAGGAACTAAACACCAAGTTAAATTAGATATACCA

>PaeR7I

>AvaI

>Asp718

>SspI >DraI

>XbaI

>ApaI >KpnI

2260

2280

2300

AAAAAAATTTCTTAAATTAACTATAAAAAAAAAAACTCGAGGGGGGGCCCGGTACC
TTTTTTATAAGAAATTAAATTGATATTTTTTTTGAGCTCCCCCCCAGGATGG

FIGURE 7D

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* 10 * 20 * 30 * 40 * 50 * 60
 GGGTGATTGACTAAATTTTAAAAATTTGAAGGTTTAAATGAGAATTTTAAACAATT
 * 70 * 80 * 90 * 100 * 110 * 120
 TTGTATGTTAACTAAACTTCAAAAAAATTTGAAGGTTAATGAGAATTTAAAAA
 * 130 * 140 * 150 * 160 * 170 * 180
 ATTTTGAGCGGGCTAATTAATTTAAAAATGTATAATAAAAAAATTCAAAAACCTCT
 >Apal
 |
 190 200 | 210 220 230 240
 TTGAGGCCATAAAGGTCATGGGCCCTAAATACATCAGCTGTTGTTCCATATTAC
 >HpaI
 |
 250 | 260 270 280 290 300
 TCATGTTATTCAGTTAACAGATATAATGGCTATCATTGATTTAGGAGTCATCTAA
 >PacI
 |
 310 320 330 340 350 360
 AATTCGAAAAGTATAAAAACAAAAAGGATTAATTGAAGAACATTAATTAAATCAACAA
 >HpaI
 |
 370 380 390 400 410 420
 TTTACTATTCCAATAACAGAATTTGAGTTAACAAATTAACTGCTACAAATTGGTTCGA
 >BclI
 |
 430 440 450 460 | 470 480
 GACCAAAATTACAAACCCGAAAAGTATTGGGACTAAATTGATCAAATTAGAGTACATG
 * 490 * 500 * 510 * 520 * 530 * 540
 GGTTAAATTACAACTTACTTATGGTACAAGGATTAATAGCATAATTCTCCTTAGGCAA
 >Hind3
 |
 550 560 570 580 590 600
 ATGCCAGTTAGTTAAAGATGTACCTTGCCCCACCGAAAGCTTCCTTAAACTCCCGCAAT
 >Hind3
 |
 610 620 630 640 | 650 660
 TTTTTAAATTCTTTTCCCTTAGAAAAAGAACAAAAATGTAGCTTGTGCTGAGAG
 * 670 * 680 * 690 * 700 * 710 * 720

FIGURE 8A

ATTTCTCTGAAATACATTGACACCAACAACCTACCCCTCCATTACACTACCAACCGGCCT
 * * * * * * * * * * * *
 730 740 750 760 770 780
 TCCCCCTTCAACTTTCTTCACCATTACAACATGCCATCTCCACCCCTAGCCAACATGC
 * * * * * * * * * * * *
 790 800 810 820 830 840
 ACTTATATCTTGTTGGTTGTTCTTTCATATAAAAACACACACRAGACACAA
 * * * * * * * * * * * *
 850 860 870 880 890 900
 [REDACTED]
 * * * * * * * * * * * *
 910 920 930 940 950 960
 GGTGTTCTCAAGGAAGAAGAAGGAGAAAGATAAGTACTTTTTGAGAATGATGGAAT
 * * * * * * * * * * * *
 >EcoRI
 970 980 990 1000 1010 | 1020
 CTGGGGTTCTGTTGCCACACTTGTGGTAACATGTTGGGTGAATGTAAGCCGAATC
 * * * * * * * * * * * *
 >SpeI >BamH1 >Asp718
 1030 1040 1050 1060
 * * * * | * | * | *
 CAGCACACTGGCGGCCGTTACTAGTGGATCCCGCGCTCGGTACC

FIGURE 8B

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PCT

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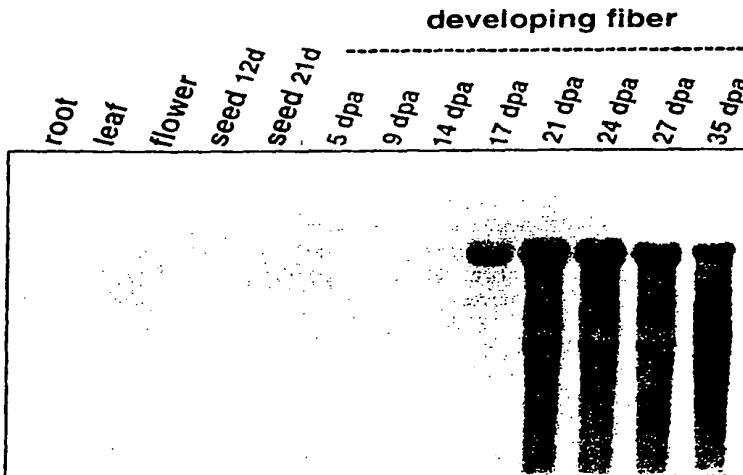
INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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			(43) International Publication Date: 7 May 1998 (07.05.98)
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(71) Applicant (for all designated States except US): CALGENE, INC. [US/US]; 1920 Fifth Street, Davis, CA 95616 (US).			
(72) Inventors; and			
(75) Inventors/Applicants (for US only): STALKER, David, M. [US/US]; 870 W. Southwood, Woodland, CA 95695 (US). PEAR, Julie, R. [US/US]; 818 Douglass Avenue, Davis, CA 95616 (US). DELMER, Deborah, P. [US/US]; 29 West Mill Street, New Palestine, IN 46163 (US).			
(74) Agents: SCHWEDLER, Carl, J. et al.; Calgene, Inc., 1920 Fifth Street, Davis, CA 95616 (US).			

(54) Title: PLANT CELLULOSE SYNTHASE AND PROMOTER SEQUENCES

(57) Abstract

Provided are two plant cDNA clones that are homologs of the bacterial CelA genes that encode the catalytic subunit of cellulose synthase, derived from cotton (*Gossypium hirsutum*). Also provided are genomic promoter regions to these encoding regions to cellulose synthase. Methods for using cellulose synthase in cotton fiber and wood quality modification are also provided.



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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/19529

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/82 C12N9/10 C12N15/29 C12N15/54 C12Q1/68
A01H5/00

According to International Patent Classification(IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C12Q A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	AMOR, Y., ET AL.: "EVIDENCE FOR A CYCLIC DIGUANYLIC ACID-DEPENDENT CELLULOSE SYNTHASE IN PLANTS" THE PLANT CELL, vol. 3, 1991, pages 989-995, XP002061420 PAGES 989, RIGHT COLUMN, PAGE 990, RIGHT COLUMN; FIG. 3 ; PAGE 993, RIGHT COLUMN - PAGE 994 ---	1-7
X	WO 91 13988 A (UNIV TEXAS) 19 September 1991 pages 1,5,7,13,18,26,46-49; claim 46 ---	1-7, 13-18,20 -/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

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1

Date of the actual completion of the international search

3 April 1998

Date of mailing of the international search report

24/04/1998

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl.
Fax: (+31-70) 340-3016

Authorized officer

Holtorf, S

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/19529

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MARTIN, T., ET AL.: "EXPRESSION OF AN ARABIDOPSIS SUCROSE SYNTHASE GENE INDICATES A ROLE IN METABOLIZATION OF SUCROSE BOTH DURING PHLOEM LOADING AND IN SINK ORGANS" THE PLANT JOURNAL, vol. 4, no. 2, 1993, pages 367-377, XP002061421 [REDACTED] - P00T - COLUMN 1 - PAGE 375 - FIG. 1	1,8,13, 15,16
X	MARTIN, T., ET AL.: "EXPRESSION OF AN ARABIDOPSIS SUCROSE SYNTHASE GENE INDICATES A ROLE IN METABOLIZATION OF SUCROSE BOTH DURING PHLOEM LOADING AND IN SINK ORGANS" EMBL SEQUENCE DATA LIBRARY, 28 December 1993, HEIDELBERG, GERMANY, XP002061422 ACCESSION NO. X70990	1,8
A	US 5 122 466 A (STOMP ANNE-MARIE ET AL) 16 June 1992 column 4 + 5	1-22
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A	DELMER, D.P., ET AL. : "CELLULOSE BIOSYNTHESIS" THE PLANT CELL, vol. 7, 1995, pages 987-1000, XP002061423 see the whole document	1-22
P,X	PEAR, J.R., ET AL. : "HIGHER PLANTS CONTAIN HOMOLOGS OF THE BACTERIAL celA GENES ENCODING THE CATALYTIC SUBUNIT OF CELLULOSE SYNTHASE" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 93, October 1996, pages 12637-12642, XP002061424 see the whole document	1-7
E	WO 98 00549 A (WILLIAMSON RICHARD EDWARD ; PENG LIANGCAI (AU); ARIOLI ANTONIO (AU)) 8 January 1998 pages 1,2,4,5,26; examples 1,2,14	1-3, 13-20

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International Application No

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